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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/989,729	11/19/2001	Avi J. Ashkenazi	10466/257	1094

35489 7590 03/09/2004

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EXAMINER	
LANDSMAN, ROBERT S	

ART UNIT	PAPER NUMBER
1647	

DATE MAILED: 03/09/2004

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	09/989,729	GENENTECH, INC.	
	Examiner	Art Unit	
	Robert Landsman	1647	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☐ Responsive to communication(s) filed on _____.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *119-138* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *119-138* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on *19 November 2001* is/are: a)☒ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date *5/24/02*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☒ Other: Sequence Comparisons A+D

DETAILED ACTION

1. Formal Matters

A. The Preliminary Amendment dated 11/19/01, has been entered into the record.

B. Claims 119-138 are pending and are the subject of this Office Action.

2. Priority

Due to the excessive number of applications from which the present application claims benefit, priority cannot be determined. However, the Examiner has concluded that the subject matter defined in this application is not supported by any of the applications in the chain of priority because the presently claimed subject matter is not supported by a specific, substantial or well-established utility, nor, for this reason, is it enabled. Accordingly, the subject matter defined in claims 119-138 has an effective filing date of 11/19/01, which is the filing date of the present application.

Should the applicant disagree with the examiner's factual determination above, it is incumbent upon the applicant to provide the serial number and specific page number(s) of any parent application filed prior to 11/19/01 which specifically supports the particular claim limitation for each and every claim limitation in all the pending claims which applicant considers to have been in possession of and fully enabled for prior to 11/19/01.

3. Information Disclosure Statement

A. References A1 and A2 on the IDS dated 5/24/02 have been lined through since they are not in proper format, including author and date of deposit.

4. Specification

A. Though none could be found, due to the length of the specification, Applicants are reminded that embedded hyperlink and/or other form of browser-executable code are not permitted in the specification. See MPEP § 608.01.

B. The title of the invention is not descriptive. A new title is required that is clearly indicative of the invention to which the claims are directed. The title recites polypeptides and polynucleotides whereas the claims are drawn to polynucleotides.

5. Claim Objections

A. The syntax of claims 119-131 could be improved by replacing the phrase "shown in Figure 228 (SEQ ID NO:314)" with "of SEQ ID NO:314" and "shown in Figure 227 (SEQ ID NO:313)" with "of SEQ ID NO:313."

6. Claim Rejections - 35 USC § 101

35 U.S.C. 101 reads as follows:

> Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

A. Claims 119-138 are rejected under 35 U.S.C. 101 because the claimed invention is not supported by a specific, substantial and credible asserted utility or a well established utility. These claims are directed to polynucleotides having various sequence homology to SEQ ID NO:313. However, the invention encompassed by these claims has no apparent or disclosed patentable utility. This rejection is consistent with the current utility guidelines, published 1/5/01, 66 FR 1092. The instant application has provided a description of an isolated protein. However, the instant application does not disclose a specific and substantial biological role of this protein or its significance.

However, it is clear from the instant specification that the claimed polynucleotide encodes a protein which is termed an "orphan receptor" in the art. The instant application does not disclose the biological role of the claimed polynucleotide, protein or their significance. Applicants disclose in the specification that the encoded receptor has certain amino acid sequence identity with microfibril-associated glycoprotein 4 (MFA4 HUMAN); ficolin-A - Mus musculus (M0078131); human lectin P35 (D63155561); ficolin B - Mus musculus (AF00632171); human tenascin-R (restriction) (HS518E13 1); the long form of a rat janusin precursor (A45445); fibrinogen-related protein HFREP-I precursor (JNO596); a human Tenascin precursor (TENA HUMAN); hllman CDT6 (HSY16132 1); and angiopoietin-l - Mus musculus (MM1.183509 1). Therefore, Applicants believe that NL7 disclosed the present application is a novel TIE ligand homologue, and may play a role in angiogenesis and/or vascular maintenance and/or wound healing and/or inflammation and/or tumor development and/or growth. However, homology alone is not sufficient to demonstrate utility of the present invention. There is little doubt that, after complete characterization, this protein will probably be found to have a patentable utility. This further characterization, however, is part of the act of invention and, until it has been undertaken, Applicants' claimed invention is incomplete.

The instant situation is directly analogous to that of which was addressed in Brenner v. Manson, 148 U.S.P.Q. 689 (Sus. Ct, 1966), in which a novel compound which was structurally analogous to other compounds which were known to possess anticancer activity was alleged to be potentially useful as an antitumor agent in the absence of evidence supporting this utility. The court expressed the opinion that all chemical compounds are "useful" to the chemical arts when this term is given its broadest interpretation. However, the court held that this broad interpretation was not the intended definition of "useful" as it appears in 35 U.S.C. 101, which required that an invention must have either an immediate obvious or fully disclosed "real-world" utility. The court held that:

> "The basic quid pro quo contemplated by the Constitution and the Congress for granting a patent monopoly is the benefit derived by the public from an invention with substantial utility," "[u]nless and until a process is refined and developed to this point - where specific benefit exists in currently available form – there is insufficient justification for permitting an applicant to engross what may prove to be a broad field," and "a patent is not a hunting license," "[i]t is not a reward for the search, but compensation for its successful conclusion."

The specification discloses that the polynucleotides of the invention encode proteins which have significant sequence similarity to known proteins. Based on the structural similarity, the specification asserts that the newly disclosed SEQ ID NO:313 has similar activities. The assertion that the disclosed proteins have biological activities similar to known polynucleotides and proteins cannot be accepted in the absence of supporting evidence, because generally, the art acknowledges that function cannot be predicted based solely on structural similarity to a protein found in the sequence databases. For example, Skolnick et al. (2000, Trends in Biotech. 18:34-39) state that knowing the protein structure by itself is insufficient to annotate a number of functional classes, and is also insufficient for annotating the specific details of protein function (see Box 2, p. 36). Similarly, Bork (2000, Genome Research 10:398-400) states that the error rate of functional annotations in the sequence database is considerable, making it even more difficult to infer correct function from a structural comparison of a new sequence with a sequence database (see especially p. 399). Such concerns are also echoed by Doerks et al. (1998, Trends in Genetics 14:248-250) who state that (1) functional information is only partially annotated in the database, ignoring multi functionality, resulting in underpredictions of functionality of a new protein and (2) overpredictions of functionality occur because structural similarity often does not necessarily coincide with functional similarity. Smith et al. (1997, Nature Biotechnology 15:1222-1223) remark that there are numerous cases in which proteins having very different functions share structural similarity due to evolution from a common ancestral gene.

Brenner (1999, Trends in Genetics 15:132-133) argues that accurate inference of function from homology must be a difficult problem since, assuming there are only about 1000 major gene superfamilies in nature, then most homologs must have different molecular and cellular functions. Finally, Bork et al. (1996, Trends in Genetics 12:425-427) add that the software robots that assign functions to new proteins often assign a function to a whole new protein based on structural similarity of a small domain of the new protein to a small domain of a known protein. Such questionable interpretations are written into the sequence database and are then considered facts.

Therefore, based on the discussions above concerning the specific examples of structurally similar proteins that have different functions, along with the art's recognition that one cannot rely upon structural similarity alone to determine functionality, the specification fails to teach the skilled artisan the utility of the polynucleotide of SEQ ID NO:313, or of the protein of SEQ ID NO:314, which is only known to be homologous to various receptors. Therefore, the instant claims are drawn to a polynucleotide encoding a protein which has a yet undetermined function or biological significance. There is no actual and specific significance which can be attributed to said protein or polynucleotide identified in the specification. For this reason, the instant invention is incomplete. In the absence of a knowledge of the natural ligands or biological significance of this protein, there is no immediately obvious patentable use for it, or for its encoding polynucleotide. To employ a protein of the instant invention in the identification of substances which bind to and/or mediate activity of the said receptor is clearly to use it as the object of further research which has been determined by the courts to be a non-patentable utility. Since the instant specification does not disclose a "real-world" use for said protein then the claimed invention is incomplete and, therefore, does not meet the requirements of 35 U.S.C. 101 as being useful.

Furthermore, since the protein of the invention is not supported by a specific and substantial asserted utility or a well established utility, the encoding polynucleotides, vectors, host cells and methods of making the protein also lack utility.

7. Claim Rejections - 35 USC § 112, first paragraph - enablement

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

A. Claims 119-138 are rejected under 35 U.S.C. 112, first paragraph, as failing to adequately teach how to use the instant invention. Specifically, since the claimed invention is not supported by a specific,

substantial and credible asserted utility or a well established utility for the reasons set forth above, one skilled in the art clearly would not know how to use the claimed invention.

B. Claims 119-138 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

The deposit of the biological material is considered necessary for the enablement of the current invention (see MPEP Chapter 2400 and 37 C.F.R. §§ 1.801-1.809). Elements required for practicing a claimed invention must be known and readily available to the public or obtainable by a repeatable method set forth in the specification. If a deposit (203128) is made under the terms of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purposes of Patent Procedure (e.g. see 961 OG 21, 1977), and Applicants, their assignee or their agent needs to provide a declaration containing the following:

1. the current address of the ATCC.
2. a declaration, or statement over attorney's signature stating that all restrictions imposed by the depositor on the availability to the public of the deposited biological material be irrevocably removed upon the granting of the patent (see MPEP Chapter 2410.01 and 37 C.F.R. § 1.808.

C. Furthermore, even if the claims possessed utility under 35 USC 101, claims 119-138 would still be rejected under 35 USC 112, first paragraph, because the specification, while then being enabling for SEQ ID NO:313 and 314, does not reasonably provide enablement for polynucleotides or polypeptides having at least 80%, 85%, 90%, 95% or 99% sequence identity to SEQ ID NO:313 or 314, to the protein encoded by ATCC No. 203128, for the extracellular domain thereof, or for vectors and host cells containing these polynucleotides. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make the invention commensurate in scope with these claims. There is no functional limitation in the claims. The claims encompass an unreasonable number of inoperative polypeptides, or polynucleotides which encode these polypeptides, which the skilled artisan would not know how to use.

There are no working examples of polynucleotides or polypeptides less than 100% identical to SEQ ID NO:313 or 314, or the mature form thereof (i.e. lacking its signal peptide). The skilled artisan would not know how to use non-identical polypeptides or polynucleotides on the basis of teachings in the prior art or specification unless they possessed a specific function disclosed in the instant specification, in which there is none. While the specification generally describes homologous proteins, Applicants still

have not taught to which family of proteins the protein of the present invention belongs. The specification does not provide guidance for using polynucleotides encoding polypeptides related to (*i.e.*, 80%-99% identity) but not identical to SEQ ID NO:313 or 314 which do not have any specific, known function. The claims are broad because they do not require the claimed polypeptide to be identical to the disclosed sequence and because the claims have no functional limitation.

For these reasons, which include the complexity and unpredictability of the nature of the invention and art in terms of the diversity of proteines and lack of knowledge about function(s) of encompassed polypeptides structurally related to SEQ ID NO:314, or their encoding polynucleotides (e.g. SEQ ID NO:313) the lack of direction or guidance for using polypeptides that are not identical to SEQ ID NO:314, and the breadth of the claims for structure without function, it would require undue experimentation to use the invention commensurate in scope with the claims.

8. Claim Rejections - 35 USC § 112, first paragraph – written description

A. Claims 119-138 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The claims are drawn to polynucleotides having at least 80%, 85%, 90%, 95% or 99% sequence identity with SEQ ID NO:313 as well as vectors and host cells. The claims do not require that the polynucleotides or encoded polypeptides of the present invention possess any particular biological activity, nor any particular conserved structure, or other disclosed distinguishing feature. Thus, the claims are drawn to a genus of polypeptides that is defined only by sequence identity.

To provide adequate written description and evidence of possession of a claimed genus, the specification must provide sufficient distinguishing identifying characteristics of the genus. The factors to be considered include disclosure of compete or partial structure, physical and/or chemical properties, functional characteristics, structure/function correlation, methods of making the claimed product, or any combination thereof. In this case, the only factor present in the claim is a partial structure in the form of a recitation of percent identity. There is not even identification of any particular portion of the structure that must be conserved. Accordingly, in the absence of sufficient recitation of distinguishing identifying characteristics, the specification does not provide adequate written description of the claimed genus.

Vas-Cath Inc. v. Mahurkar, 19USPQ2d 1111, clearly states "applicant must convey with reasonable clarity to those skilled in the art that, as of the filing date sought, he or she was in possession

of the invention. The invention is, for purposes of the 'written description' inquiry, *whatever is now claimed.*" (See page 1117.) The specification does not "clearly allow persons of ordinary skill in the art to recognize that [he or she] invented what is claimed." (See *Vas-Cath* at page 1116). As discussed above, the skilled artisan cannot envision the detailed chemical structure of the encompassed genus of polypeptides, and therefore conception is not achieved until reduction to practice has occurred, regardless of the complexity or simplicity of the method of isolation. Adequate written description requires more than a mere statement that it is part of the invention and reference to a potential method of isolating it. The compound itself is required. See *Fiers v. Revel*, 25 USPQ2d 1601 at 1606 (CAFC 1993) and *Amgen Inc. v. Chugai Pharmaceutical Co. Ltd.*, 18 USPQ2d 1016.

One cannot describe what one has not conceived. See *Fiddes v. Baird*, 30 USPQ2d 1481 at 1483. In *Fiddes*, claims directed to mammalian FGF's were found to be unpatentable due to lack of written description for that broad class. The specification provided only the bovine sequence.

Therefore, only isolated polypeptides comprising the amino acid sequence set forth in SEQ ID NO:314, or encoded by SEQ ID NO:313, but not the full breadth of the claims, meets the written description provision of 35 U.S.C. §112, first paragraph. Applicant is reminded that *Vas-Cath* makes clear that the written description provision of 35 U.S.C. §112 is severable from its enablement provision (see page 1115).

9. Claim Rejections - 35 USC § 112, second paragraph

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 119-138 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

A. Claims 119-138 are vague and indefinite since it is not clear whether or not the protein encoded by the polynucleotide of the present invention is a soluble protein (e.g protease), nor is it disclosed as being expressed on a cell surface. Accordingly, the limitation that the claimed protein comprises an "extracellular domain" is indefinite, as the art does not recognize soluble proteins as having such domains. Further, if the protein had an extracellular domain, the recitation of "the extracellular domain"..."lacking its associated signal sequence" is indefinite as a signal sequence is not generally considered to be part of an extracellular domain, as signal sequences are cleaved from said domains in the process of secretion from the cell.

B. Claims 132-134 are vague and indefinite since the claim recites "hybridizes" without the recitation of any conditions, or recites "stringent conditions: wherein these conditions are not known. Nucleic acid molecules which hybridize under conditions of "low" stringency would not necessarily hybridize under conditions of "high" stringency. Furthermore, not all conditions of "high" or "low" stringency, for example, are the same. Therefore, it is required that Applicants amend the claims to recite the exact hybridization conditions without using indefinite phrases such as "*for example*" **without adding new matter**.

10. Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

A. Claims 119-138 are rejected under 35 U.S.C. 102(b) as being anticipated by Baker et al. (WO 99/63088. The claims recite a polynucleotide at least 80% identical to that of SEQ ID NO:313 or encoding 314, as well as fragments thereof. The claims also recite nucleic acid molecules which hybridize to SEQ ID NO:313, or one encoding SEQ ID NO:314 as well as vectors and host cells. Baker teach a polynucleotide which is 100% identical to SEQ ID NO:313 (Sequence Comparisons A-C) as well as vectors and host cells (pages 352-355). This nucleic acid molecule will hybridize to that of the present invention even under the most stringent conditions.

B Claims 132-134 are rejected under 35 U.S.C. 102(b) as being anticipated by Fernandez et al. (WO 00/061754. The claims recite a nucleic acid molecule which hybridizes to SEQ ID NO:313, or one encoding SEQ ID NO:314. Fernandez teach a polynucleotide which is 100% identical over approximately 1070 contiguous bases (Sequence Comparison D). This nucleic acid molecule will hybridize to that of the present invention even under the most stringent conditions.

11. Conclusion

A. No claim is allowable.

Advisory information

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Robert Landsman whose telephone number is (703) 306-3407. The examiner can normally be reached on Monday - Friday from 8:00 AM to 5:00 PM (Eastern time) and alternate Fridays from 8:00 AM to 5:00 PM (Eastern time).

If attempts to reach the examiner by telephone are unsuccessful, the Examiner's supervisor, Gary Kunz, can be reached on (703) 308-4623.

Official papers filed by fax should be directed to (703) 308-4242. Fax draft or informal communications with the examiner should be directed to (703) 308-0294.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the Group receptionist whose telephone number is (703) 308-0196.

Robert Landsman, Ph.D.
Patent Examiner
Group 1600
March 05, 2004

ROBERT LANDSMAN
PATENT EXAMINER

Sequence Comparison A

```
ID   AAY66727 standard; protein; 461 AA.
XX
DT   05-APR-2000  (first entry)
XX
DE   Membrane-bound protein PRO1346.
XX
KW   Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW   pharmaceutical; receptor immunoadhesin; gene mapping.
XX
OS   Homo sapiens.
XX
PN   WO9963088-A2.
XX
PD   09-DEC-1999.
XX
PF   02-JUN-1999;   99WO-US12252.
XX
PR   02-JUN-1998;   98US-0087607.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker K,  Chen J,  Goddard A,  Gurney AL,  Smith V,  Watanabe CK;
PI   Wood WI,  Yuan J;
XX
DR   WPI; 2000-072883/06.
DR   N-PSDB; AAZ65071.
XX
PT   Membrane-bound proteins and related nucleotide sequences  -
XX
PS   claim 12; Fig 228; 822pp; English.
XX
CC   The invention provides membrane-bound PRO polypeptides and
CC   polynucleotides encoding them. The PRO sequences of the invention were
CC   identified based on extracellular domain homology screening. The PRO
CC   sequences have homology with proteins including LDL receptors, TIE
CC   ligands and various enzymes. The membrane-bound proteins and receptor
CC   molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC   immunoadhesins, for instance, can be used as therapeutic agents to block
CC   receptor-ligand interactions. The membrane-bound proteins can also be
CC   employed for screening of potential peptide or small molecule inhibitors
CC   of the relevant receptor/ligand interaction. The PRO encoding sequences
CC   are useful as hybridization probes, in chromosome and gene mapping and in
CC   the generation of antisense RNA and DNA. PRO nucleic acid sequences
CC   will also be useful for the preparation of PRO polypeptides, especially
CC   by recombinant techniques.
XX
SQ   Sequence   461 AA;

  Query Match             100.0%;  Score 2450;  DB 21;  Length 461;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-225;
  Matches  461;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MVNDRWKTMGGAAQLEDRPRDKPQRPSCGYVLCTVLLALAVLLAVAVTGAVLFLNHAHAP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MVNDRWKTMGGAAQLEDRPRDKPQRPSCGYVLCTVLLALAVLLAVAVTGAVLFLNHAHAP 60

Qy         61 GTAPPPVVSTGAASANSALVTVERADSSHLSILIDPRCPDLTDSFARLESAQASVLQALT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTAPPPVVSTGAASANSALVTVERADSSHLSILIDPRCPDLTDSFARLESAQASVLQALT 120

Qy        121 EHQAQPRLVGDQEQELLDTLADQLPRLLARASELQTECMGLRKGHGTLGQGLSALQSEQG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EHQAQPRLVGDQEQELLDTLADQLPRLLARASELQTECMGLRKGHGTLGQGLSALQSEQG 180
```

```
Qy        181 RLIQLLSESQGHMAHLVNSVSDILDALQRDRGLGRPRNKADLQRAPARGTRPRGCATGSR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RLIQLLSESQGHMAHLVNSVSDILDALQRDRGLGRPRNKADLQRAPARGTRPRGCATGSR 240

Qy        241 PRDCLDVLLSGQQDDGVYSVFPTHYPAGFQVYCDMRTDGGGWTVFQRREDGSVNFFRGWD 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PRDCLDVLLSGQQDDGVYSVFPTHYPAGFQVYCDMRTDGGGWTVFQRREDGSVNFFRGWD 300

Qy        301 AYRDGFGRLTGEHWLGLKRIHALTTQAAYELHVDLEDFENGTAYARYGSFGVGLFSVDPE 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AYRDGFGRLTGEHWLGLKRIHALTTQAAYELHVDLEDFENGTAYARYGSFGVGLFSVDPE 360

Qy        361 EDGYPLTVADYSGTAGDSLLKHSGMRFTTKDRDSDHSENNCAAFYRGAWWYRNCHTSNLN 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 EDGYPLTVADYSGTAGDSLLKHSGMRFTTKDRDSDHSENNCAAFYRGAWWYRNCHTSNLN 420

Qy        421 GQYLRGAHASYADGVEWSSWTGWQYSLKFSEMKIRPVREDR 461
              |||||||||||||||||||||||||||||||||||||||||
Db        421 GQYLRGAHASYADGVEWSSWTGWQYSLKFSEMKIRPVREDR 461
```

Sequence Comparison B

```
ID   AAZ65071 standard; cDNA; 3010 BP.
XX
PN   WO9963088-A2.
XX
PD   09-DEC-1999.
XX
SQ   Sequence 3010 BP; 497 A; 1045 C; 938 G; 530 T; 0 other;
```

Alignment Scores:

Pred. No.:	1.09e-191	Length:	3010
Score:	2450.00	Matches:	461
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	21	Gaps:	0

US-09-989-729A-314 (1-461) x AAZ65071 (1-3010)

```
Qy          1 MetValAsnAspArgTrpLysThrMetGlyGlyAlaAlaGlnLeuGluAspArgProArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTCAACGACCGGTGGAAGACCATGGGCGGCGCTGCCCAACTTGAGGACCGGCCGCGC 60

Qy         21 AspLysProGlnArgProSerCysGlyTyrValLeuCysThrValLeuLeuAlaLeuAla 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GACAAGCCGCAGCGGCCGAGCTGCGGCTACGTGCTGTGCACCGTGCTGCTGGCCCTGGCT 120

Qy         41 ValLeuLeuAlaValAlaValThrGlyAlaValLeuPheLeuAsnHisAlaHisAlaPro 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTGCTGCTGGCTGTAGCTGTCACCGGTGCCGTGCTCTTCCTGAACCACGCCCACGCGCCG 180

Qy         61 GlyThrAlaProProProValValSerThrGlyAlaAlaSerAlaAsnSerAlaLeuVal 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGCACGGCGCCCCCACCTGTCGTCAGCACTGGGGCTGCCAGCGCCAACAGCGCCCTGGTC 240

Qy         81 ThrValGluArgAlaAspSerSerHisLeuSerIleLeuIleAspProArgCysProAsp 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACTGTGGAAAGGGCGGACAGCTCGCACCTCAGCATCCTCATTGACCCGCGCTGCCCCGAC 300
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B cont'd

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Qy        101 LeuThrAspSerPheAlaArgLeuGluSerAlaGlnAlaSerValLeuGlnAlaLeuThr 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTCACCGACAGCTTCGCACGCCTGGAGAGCGCCCAGGCCTCGGTGCTGCAGGCGCTGACA 360

Qy        121 GluHisGlnAlaGlnProArgLeuValGlyAspGlnGluGlnGluLeuLeuAspThrLeu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAGCACCAGGCCCAGCCACGGCTGGTGGGCGACCAGGAGCAGGAGCTGCTGGACACGCTG 420

Qy        141 AlaAspGlnLeuProArgLeuLeuAlaArgAlaSerGluLeuGlnThrGluCysMetGly 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCCGACCAGCTGCCCCGGCTGCTGGCCCGAGCCTCAGAGCTGCAGACGGAGTGCATGGGG 480

Qy        161 LeuArgLysGlyHisGlyThrLeuGlyGlnGlyLeuSerAlaLeuGlnSerGluGlnGly 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTGCGGAAGGGGCATGGCACGCTGGGCCAGGGCCTCAGCGCCCTGCAGAGTGAGCAGGGC 540

Qy        181 ArgLeuIleGlnLeuLeuSerGluSerGlnGlyHisMetAlaHisLeuValAsnSerVal 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CGCCTCATCCAGCTTCTCTCTGAGAGCCAGGGCCACATGGCTCACCTGGTGAACTCCGTC 600

Qy        201 SerAspIleLeuAspAlaLeuGlnArgAspArgGlyLeuGlyArgProArgAsnLysAla 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCGACATCCTGGATGCCCTGCAGAGGGACCGGGGGCTGGGCCGGCCCCGCAACAAGGCC 660

Qy        221 AspLeuGlnArgAlaProAlaArgGlyThrArgProArgGlyCysAlaThrGlySerArg 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GACCTTCAGAGAGCGCCTGCCCGGGGAACCCGGCCCCGGGGCTGTGCCACTGGCTCCCGG 720

Qy        241 ProArgAspCysLeuAspValLeuLeuSerGlyGlnGlnAspAspGlyValTyrSerVal 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CCCCGAGACTGTCTGGACGTCCTCCTAAGCGGACAGCAGGACGATGGCGTCTACTCTGTC 780

Qy        261 PheProThrHisTyrProAlaGlyPheGlnValTyrCysAspMetArgThrAspGlyGly 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTTCCCACCCACTACCCGGCCGGCTTCCAGGTGTACTGTGACATGCGCACGGACGGCGGC 840

Qy        281 GlyTrpThrValPheGlnArgArgGluAspGlySerValAsnPhePheArgGlyTrpAsp 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGCTGGACGGTGTTTCAGCGCCGGGAGGACGGCTCCGTGAACTTCTTCCGGGGCTGGGAC 900

Qy        301 AlaTyrArgAspGlyPheGlyArgLeuThrGlyGluHisTrpLeuGlyLeuLysArgIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCGTACCGAGACGGCTTTGGCAGGCTCACCGGGGAGCACTGGCTAGGGCTCAAGAGGATC 960

Qy        321 HisAlaLeuThrThrGlnAlaAlaTyrGluLeuHisValAspLeuGluAspPheGluAsn 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CACGCCCTGACCACACAGGCTGCCTACGAGCTGCACGTGGACCTGGAGGACTTTGAGAAT 1020

Qy        341 GlyThrAlaTyrAlaArgTyrGlySerPheGlyValGlyLeuPheSerValAspProGlu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGCACGGCCTATGCCCGCTACGGGAGCTTCGGCGTGGGCTTGTTCTCCGTGGACCCTGAG 1080

Qy        361 GluAspGlyTyrProLeuThrValAlaAspTyrSerGlyThrAlaGlyAspSerLeuLeu 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GAAGACGGGTACCCGCTCACCGTGGCTGACTATTCCGGCACTGCAGGCGACTCCCTCCTG 1140

Qy        381 LysHisSerGlyMetArgPheThrThrLysAspArgAspSerAspHisSerGluAsnAsn 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AAGCACAGCGGCATGAGGTTCACCACCAAGGACCGTGACAGCGACCATTCAGAGAACAAC 1200

Qy        401 CysAlaAlaPheTyrArgGlyAlaTrpTrpTyrArgAsnCysHisThrSerAsnLeuAsn 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TGTGCCGCCTTCTACCGCGGTGCCTGGTGGTACCGCAACTGCCACACGTCCAACCTCAAT 1260
```

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Qy        421 GlyGlnTyrLeuArgGlyAlaHisAlaSerTyrAlaAspGlyValGluTrpSerSerTrp 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GGGCAGTACCTGCGCGGTGCGCACGCCTCCTATGCCGACGGCGTGGAGTGGTCCTCCTGG 1320

Qy        441 ThrGlyTrpGlnTyrSerLeuLysPheSerGluMetLysIleArgProValArgGluAsp 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ACCGGCTGGCAGTACTCACTCAAGTTCTCTGAGATGAAGATCCGGCCGGTCCGGGAGGAC 1380

Qy        461 Arg 461
              |||
Db       1381 CGC 1383
```

Sequence comparism C

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ID   AAZ65071 standard; cDNA; 3010 BP.
XX
PN   WO9963088-A2.
XX
PD   09-DEC-1999.

SQ   Sequence 3010 BP; 497 A; 1045 C; 938 G; 530 T; 0 other;

  Query Match           100.0%;  Score 3010;  DB 21;  Length 3010;
  Best Local Similarity 100.0%;  Pred. No. 0;
  Matches 3010;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGTCAACGACCGGTGGAAGACCATGGGCGGCGCTGCCCAACTTGAGGACCGGCCGCGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTCAACGACCGGTGGAAGACCATGGGCGGCGCTGCCCAACTTGAGGACCGGCCGCGC 60

Qy         61 GACAAGCCGCAGCGGCCGAGCTGCGGCTACGTGCTGTGCACCGTGCTGCTGGCCCTGGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GACAAGCCGCAGCGGCCGAGCTGCGGCTACGTGCTGTGCACCGTGCTGCTGGCCCTGGCT 120

Qy        121 GTGCTGCTGGCTGTAGCTGTCACCGGTGCCGTGCTCTTCCTGAACCACGCCCACGCGCCG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTGCTGCTGGCTGTAGCTGTCACCGGTGCCGTGCTCTTCCTGAACCACGCCCACGCGCCG 180

Qy        181 GGCACGGCGCCCCCACCTGTCGTCAGCACTGGGGCTGCCAGCGCCAACAGCGCCCTGGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGCACGGCGCCCCCACCTGTCGTCAGCACTGGGGCTGCCAGCGCCAACAGCGCCCTGGTC 240

Qy        241 ACTGTGGAAAGGGCGGACAGCTCGCACCTCAGCATCCTCATTGACCCGCGCTGCCCCGAC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACTGTGGAAAGGGCGGACAGCTCGCACCTCAGCATCCTCATTGACCCGCGCTGCCCCGAC 300

Qy        301 CTCACCGACAGCTTCGCACGCCTGGAGAGCGCCCAGGCCTCGGTGCTGCAGGCGCTGACA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTCACCGACAGCTTCGCACGCCTGGAGAGCGCCCAGGCCTCGGTGCTGCAGGCGCTGACA 360

Qy        361 GAGCACCAGGCCCAGCCACGGCTGGTGGGCGACCAGGAGCAGGAGCTGCTGGACACGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAGCACCAGGCCCAGCCACGGCTGGTGGGCGACCAGGAGCAGGAGCTGCTGGACACGCTG 420

Qy        421 GCCGACCAGCTGCCCCGGCTGCTGGCCCGAGCCTCAGAGCTGCAGACGGAGTGCATGGGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCCGACCAGCTGCCCCGGCTGCTGGCCCGAGCCTCAGAGCTGCAGACGGAGTGCATGGGG 480

Qy        481 CTGCGGAAGGGGCATGGCACGCTGGGCCAGGGCCTCAGCGCCCTGCAGAGTGAGCAGGGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTGCGGAAGGGGCATGGCACGCTGGGCCAGGGCCTCAGCGCCCTGCAGAGTGAGCAGGGC 540
```

C cont'd

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Qy        541 CGCCTCATCCAGCTTCTCTCTGAGAGCCAGGGCCACATGGCTCACCTGGTGAACTCCGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CGCCTCATCCAGCTTCTCTCTGAGAGCCAGGGCCACATGGCTCACCTGGTGAACTCCGTC 600

Qy        601 AGCGACATCCTGGATGCCCTGCAGAGGGACCGGGGGCTGGGCCGGCCCCGCAACAAGGCC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCGACATCCTGGATGCCCTGCAGAGGGACCGGGGGCTGGGCCGGCCCCGCAACAAGGCC 660

Qy        661 GACCTTCAGAGAGCGCCTGCCCGGGGAACCCGGCCCCGGGGCTGTGCCACTGGCTCCCGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GACCTTCAGAGAGCGCCTGCCCGGGGAACCCGGCCCCGGGGCTGTGCCACTGGCTCCCGG 720

Qy        721 CCCCGAGACTGTCTGGACGTCCTCCTAAGCGGACAGCAGGACGATGGCGTCTACTCTGTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CCCCGAGACTGTCTGGACGTCCTCCTAAGCGGACAGCAGGACGATGGCGTCTACTCTGTC 780

Qy        781 TTTCCCACCCACTACCCGGCCGGCTTCCAGGTGTACTGTGACATGCGCACGGACGGCGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTTCCCACCCACTACCCGGCCGGCTTCCAGGTGTACTGTGACATGCGCACGGACGGCGGC 840

Qy        841 GGCTGGACGGTGTTTCAGCGCCGGGAGGACGGCTCCGTGAACTTCTTCCGGGGCTGGGAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGCTGGACGGTGTTTCAGCGCCGGGAGGACGGCTCCGTGAACTTCTTCCGGGGCTGGGAC 900

Qy        901 GCGTACCGAGACGGCTTTGGCAGGCTCACCGGGGAGCACTGGCTAGGGCTCAAGAGGATC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCGTACCGAGACGGCTTTGGCAGGCTCACCGGGGAGCACTGGCTAGGGCTCAAGAGGATC 960

Qy        961 CACGCCCTGACCACACAGGCTGCCTACGAGCTGCACGTGGACCTGGAGGACTTTGAGAAT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CACGCCCTGACCACACAGGCTGCCTACGAGCTGCACGTGGACCTGGAGGACTTTGAGAAT 1020

Qy       1021 GGCACGGCCTATGCCCGCTACGGGAGCTTCGGCGTGGGCTTGTTCTCCGTGGACCCTGAG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGCACGGCCTATGCCCGCTACGGGAGCTTCGGCGTGGGCTTGTTCTCCGTGGACCCTGAG 1080

Qy       1081 GAAGACGGGTACCCGCTCACCGTGGCTGACTATTCCGGCACTGCAGGCGACTCCCTCCTG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GAAGACGGGTACCCGCTCACCGTGGCTGACTATTCCGGCACTGCAGGCGACTCCCTCCTG 1140

Qy       1141 AAGCACAGCGGCATGAGGTTCACCACCAAGGACCGTGACAGCGACCATTCAGAGAACAAC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AAGCACAGCGGCATGAGGTTCACCACCAAGGACCGTGACAGCGACCATTCAGAGAACAAC 1200

Qy       1201 TGTGCCGCCTTCTACCGCGGTGCCTGGTGGTACCGCAACTGCCACACGTCCAACCTCAAT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TGTGCCGCCTTCTACCGCGGTGCCTGGTGGTACCGCAACTGCCACACGTCCAACCTCAAT 1260

Qy       1261 GGGCAGTACCTGCGCGGTGCGCACGCCTCCTATGCCGACGGCGTGGAGTGGTCCTCCTGG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GGGCAGTACCTGCGCGGTGCGCACGCCTCCTATGCCGACGGCGTGGAGTGGTCCTCCTGG 1320

Qy       1321 ACCGGCTGGCAGTACTCACTCAAGTTCTCTGAGATGAAGATCCGGCCGGTCCGGGAGGAC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 ACCGGCTGGCAGTACTCACTCAAGTTCTCTGAGATGAAGATCCGGCCGGTCCGGGAGGAC 1380

Qy       1381 CGCTAGACTGGTGCACCTTGTCCTTGGCCCTGCTGGTCCCTGTCGCCCCATCCCCGACCC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCTAGACTGGTGCACCTTGTCCTTGGCCCTGCTGGTCCCTGTCGCCCCATCCCCGACCC 1440

Qy       1441 CACCTCACTCTTTCGTGAATGTTCTCCACCCACCTGTGCCTGGCGGACCCACTCTCCAGT 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CACCTCACTCTTTCGTGAATGTTCTCCACCCACCTGTGCCTGGCGGACCCACTCTCCAGT 1500
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Qy       1501 AGGGAGGGGCCGGGCCATCCCTGACACGAAGCTCCCTGGGCCGGTGAAGTCACACATCGC 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 AGGGAGGGGCCGGGCCATCCCTGACACGAAGCTCCCTGGGCCGGTGAAGTCACACATCGC 1560

Qy       1561 CTTCTCGCCGTCCCCACCCCCTCCATTTGGCAGCTCACTGATCTCTTGCCTCTGCTGATG 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CTTCTCGCCGTCCCCACCCCCTCCATTTGGCAGCTCACTGATCTCTTGCCTCTGCTGATG 1620

Qy       1621 GGGGCTGGCAAACTTGACGACCCCAACTCCTGCCTGCCCCCACTGTGACTCCGGTGCTGT 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GGGGCTGGCAAACTTGACGACCCCAACTCCTGCCTGCCCCCACTGTGACTCCGGTGCTGT 1680

Qy       1681 TTGCCGTCCCCTGGCCAGGATGGTGGAGTCTGCCCCAGGCACCCTCTGCCCTGCCCGGCC 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 TTGCCGTCCCCTGGCCAGGATGGTGGAGTCTGCCCCAGGCACCCTCTGCCCTGCCCGGCC 1740

Qy       1741 AAATACCCGGCATTATGGGGACAGAGAGCAGGGGGCAGACAGCACCCCTGGAGTCCTCCT 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 AAATACCCGGCATTATGGGGACAGAGAGCAGGGGGCAGACAGCACCCCTGGAGTCCTCCT 1800

Qy       1801 AGCAGATCGTGGGGAATGTCAGGTCTCTCTGAGGTCAGGTCTGAGGCCAGTATCCTCCAG 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 AGCAGATCGTGGGGAATGTCAGGTCTCTCTGAGGTCAGGTCTGAGGCCAGTATCCTCCAG 1860

Qy       1861 CCCTCCCAATGCCAACCCCCACCCCGTTTCCCTGGTGCCCAGAGAACCCACCTCTCCCCC 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 CCCTCCCAATGCCAACCCCCACCCCGTTTCCCTGGTGCCCAGAGAACCCACCTCTCCCCC 1920

Qy       1921 AAGGGCCTCAGCCTGGCTGTGGGCTGGGTGGCCCCATCCTACCAGGCCCTGAGGTCAGGA 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 AAGGGCCTCAGCCTGGCTGTGGGCTGGGTGGCCCCATCCTACCAGGCCCTGAGGTCAGGA 1980

Qy       1981 TGGGGAGCTGCTGCCTTTGGGGACCCACGCTCCAAGGCTGAGACCAGTTCCCTGGAGGCC 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 TGGGGAGCTGCTGCCTTTGGGGACCCACGCTCCAAGGCTGAGACCAGTTCCCTGGAGGCC 2040

Qy       2041 ACCCACCCTGTGCCCCGGCAGGCCTGGGGTCTGCAGTCCTCTTACCTGCTGTGCCCACCT 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 ACCCACCCTGTGCCCCGGCAGGCCTGGGGTCTGCAGTCCTCTTACCTGCTGTGCCCACCT 2100

Qy       2101 GCTCTCTGTCTCAAATGAGGCCCAACCCATCCCCCACCCAGCTCCCGGCCGTCCTCCTAC 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 GCTCTCTGTCTCAAATGAGGCCCAACCCATCCCCCACCCAGCTCCCGGCCGTCCTCCTAC 2160

Qy       2161 CTGGGGCAGCCGGGGCTGCCATCCCATTTCTCCTGCCTCTGGAAGGTGGGTGGGGCCCTG 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 CTGGGGCAGCCGGGGCTGCCATCCCATTTCTCCTGCCTCTGGAAGGTGGGTGGGGCCCTG 2220

Qy       2221 CACCGTGGGGCTGGACTGCGCTAATGGGAAGCTCTTGGTTTTCTGGGCTGGGGCCTAGGC 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 CACCGTGGGGCTGGACTGCGCTAATGGGAAGCTCTTGGTTTTCTGGGCTGGGGCCTAGGC 2280

Qy       2281 AGGGCTGGGATGAGGCTTGTACAACCCCCACCACCAATTTCCCAGGGACTCCAGGGTCCT 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 AGGGCTGGGATGAGGCTTGTACAACCCCCACCACCAATTTCCCAGGGACTCCAGGGTCCT 2340

Qy       2341 GAGGCCTCCCAGGAGGGCCTTGGGGGTGATGACCCCTTCCCTGAGGTGGCTGTCTCCATG 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 GAGGCCTCCCAGGAGGGCCTTGGGGGTGATGACCCCTTCCCTGAGGTGGCTGTCTCCATG 2400

Qy       2401 AGGAGGCCAACCCTTGCCATTGACCGTGGCCACCTGGACCCAGGCCAGGCCCGGCCCGGC 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 AGGAGGCCAACCCTTGCCATTGACCGTGGCCACCTGGACCCAGGCCAGGCCCGGCCCGGC 2460
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C cont'd

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Qy       2461 GAGTGGTCAAGGGACAGGGACCACCTCACCGGGCAAATGGGGTCGGGGGGACTGGGGCAC 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 GAGTGGTCAAGGGACAGGGACCACCTCACCGGGCAAATGGGGTCGGGGGGACTGGGGCAC 2520

Qy       2521 CAGACCAGGCACCACCTGGACACTTTCTTGTTGAATCCTCCCAACACCCAGCACGCTGTC 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 CAGACCAGGCACCACCTGGACACTTTCTTGTTGAATCCTCCCAACACCCAGCACGCTGTC 2580

Qy       2581 ATCCCCACTCCTTGTGTGCACACATGCAGAGGTGAGACCCGCAGGCTCCCAGGACCAGCA 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 ATCCCCACTCCTTGTGTGCACACATGCAGAGGTGAGACCCGCAGGCTCCCAGGACCAGCA 2640

Qy       2641 GCCACAAGGGCAGGGCTGGAGCCGGGTCCTCAGCTGTCTGCTCAGCAGCCCTGGACCCGC 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 GCCACAAGGGCAGGGCTGGAGCCGGGTCCTCAGCTGTCTGCTCAGCAGCCCTGGACCCGC 2700

Qy       2701 GTGCGTTACGTCAGGCCCAGATGCAGGGCGGCTTTTCCAAGGCCTCCTGATGGGGGCCTC 2760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 GTGCGTTACGTCAGGCCCAGATGCAGGGCGGCTTTTCCAAGGCCTCCTGATGGGGGCCTC 2760

Qy       2761 CGAAAGGGCTGGAGTCAGCCTTGGGGAGCTGCCTAGCAGCCTCTCCTCGGGCAGGAGGGG 2820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 CGAAAGGGCTGGAGTCAGCCTTGGGGAGCTGCCTAGCAGCCTCTCCTCGGGCAGGAGGGG 2820

Qy       2821 AGGTGGCTTCCTCCAAAGGACACCCGATGGCAGGTGCCTAGGGGGTGTGGGGTTCCGTTC 2880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 AGGTGGCTTCCTCCAAAGGACACCCGATGGCAGGTGCCTAGGGGGTGTGGGGTTCCGTTC 2880

Qy       2881 TCCCTTCCCCTCCCACTGAAGTTTGTGCTTAAAAAACAATAAATTTGACTTGGCACCACT 2940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 TCCCTTCCCCTCCCACTGAAGTTTGTGCTTAAAAAACAATAAATTTGACTTGGCACCACT 2940

Qy       2941 GGGGGTTGGTGGGAGAGGCCGTGTGACCTGGCTCTCTGTCCCAGTGCCACCAGGTCATCC 3000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 GGGGGTTGGTGGGAGAGGCCGTGTGACCTGGCTCTCTGTCCCAGTGCCACCAGGTCATCC 3000

Qy       3001 ACATGCGCAG 3010
             ||||||||||
Db       3001 ACATGCGCAG 3010
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Sequence Comparison D

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ID   AAA88801 standard; cDNA; 1099 BP.
XX
AC   AAA88801;
XX
DT   19-FEB-2001  (first entry)
XX
DE   Human SECX cDNA Clone 4437909.0.4.
XX
KW   SECX; human; diagnosis; gene therapy; chromosome 9;
KW   reproductive disorder; muscular disorder; immunological disorder;
KW   cancer; infection; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             83..892
FT                   /*tag=  a
XX
PN   WO200061754-A2.
XX
PD   19-OCT-2000.
XX
PF   07-APR-2000; 2000WO-US09392.
XX
PR   09-APR-1999;   99US-0128514.
PR   03-MAR-2000; 2000US-0128514.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Fernandez E,  Vernet C,  Shimkets R;
XX
DR   WPI; 2000-679487/66.
DR   P-PSDB; AAB19732.
XX
PT   SECX polypeptides and the nucleic acids that encode them, useful for
PT   diagnosing, preventing and treating e.g. cancers, inflammation,
PT   arthritis and immunological disorders -
XX
PS   Claim 10; Fig 13; 143pp; English.
XX
CC   The present sequence is that of SECX Clone 4437909.0.4, which
CC   encodes a microbody (peroxisome) associated protein (see AAB19732).
CC   The clone was found in osteogenic sarcoma cell lines, adrenal
CC   gland, thalamus, foetal brain and foetal lung.  The invention
CC   provides novel SECX polynucleotides (see AAA88789-804) and the
CC   secreted or membrane-associated proteins encoded by them (see
CC   AAB19720-34).  SECX polynucleotides, polypeptides and antibodies can
CC   be used in the detection, diagnosis and treatment (including gene
CC   therapy) of a broad range of pathological states.  The 4437909
CC   gene maps to human chromosome 9.  Clone 4437909.0.4 polypeptide
CC   shows similarity to human microfibril-associated glycoprotein 4
CC   splice variant MAG4V and may therefore be useful for treating
CC   reproductive disorders (e.g. disruptions of the oestrus cycle and
CC   spermatogenesis, polycystic ovary syndrome and cancers of the
CC   prostate and ovary), muscular disorders (e.g. Duchenne's muscular
CC   dystrophy, lipid myopathy and myocarditis), immunological
CC   disorders (e.g. Addison's disease, asthma, anaemia and AIDS) and
CC   neoplastic disorders (e.g. myeloma, sarcoma, leukaemia and lung
CC   cancer).  Similarity is also shown to human opsonin protein P35,
CC   suggesting use in the prevention and treatment of infectious
CC   diseases.  A variant clone, 4437909.0.55, is given in AAA88802,
CC   and a clone obtained by PCR amplification is gicen in AAA88804.
XX
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B cont'd

SQ Sequence 1099 BP; 188 A; 380 C; 333 G; 198 T; 0 other;

Query Match 35.1%; Score 1055.8; DB 21; Length 1099;
Best Local Similarity 99.7%; Pred. No. 1.7e-185;
Matches 1068; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Qy        524 TGCAGAGTGAGC-AGGGCCGCCTCATCCAGCTTCTCTCTGAGAGCCAGGGCCACATGGCT 582
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Db         29 TGCAGAGTGAGCAAGGGCCGCCTCATCCAGCTTCTCTCTGAGAGCCAGGGCCACATGGCT 88

Qy        583 CACCTGGTGAACTCCGTCAGCGACATCCTGGATGCCCTGCAGAGGGACCGGGGGCTGGGC 642
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 CACCTGGTGAACTCCGTCAGCGACATCCTGGATGCCCTGCAGAGGGACCGGGGGCTGGGC 148

Qy        643 CGGCCCCGCAACAAGGCCGACCTTCAGAGAGCGCCTGCCCGGGGAACCCGGCCCCGGGGC 702
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Db        149 CGGCCCCGCAACAAGGCCGACCTTCAGAGAGCGCCTGCCCGGGGAACCCGGCCCCGGGGC 208

Qy        703 TGTGCCACTGGCTCCCGGCCCCGAGACTGTCTGGACGTCCTCCTAAGCGGACAGCAGGAC 762
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        209 TGTGCCACTGGCTCCCGGCCCCGAGACTGTCTGGACGTCCTCCTAAGCGGACAGCAGGAC 268

Qy        763 GATGGCGTCTACTCTGTCTTTCCCACCCACTACCCGGCCGGCTTCCAGGTGTACTGTGAC 822
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Qy        823 ATGCGCACGGACGGCGGCGGCTGGACGGTGTTTCAGCGCCGGGAGGACGGCTCCGTGAAC 882
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Db        329 ATGCGCACGGACGGCGGCGGCTGGACGGTGTTTCAGCGCCGGGAGGACGGCTCCGTGAAC 388

Qy        883 TTCTTCCGGGGCTGGGACGCGTACCGAGACGGCTTTGGCAGGCTCACCGGGGAGCACTGG 942
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Qy        943 CTAGGGCTCAAGAGGATCCACGCCCTGACCACACAGGCTGCCTACGAGCTGCACGTGGAC 1002
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Qy       1003 CTGGAGGACTTTGAGAATGGCACGGCCTATGCCCGCTACGGGAGCTTCGGCGTGGGCTTG 1062
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Db        509 CTGGAGGACTTTGAGAATGGCACGGCCTATGCCCGCTACGGGAGCTTCGGCGTGGGCTTG 568

Qy       1063 TTCTCCGTGGACCCTGAGGAAGACGGGTACCCGCTCACCGTGGCTGACTATTCCGGCACT 1122
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Qy       1123 GCAGGCGACTCCCTCCTGAAGCACAGCGGCATGAGGTTCACCACCAAGGACCGTGACAGC 1182
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Qy       1183 GACCATTCAGAGAACAACTGTGCCGCCTTCTACCGCGGTGCCTGGTGGTACCGCAACTGC 1242
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Qy       1243 CACACGTCCAACCTCAATGGGCAGTACCTGCGCGGTGCGCACGCCTCCTATGCCGACGGC 1302
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Db        749 CACACGTCCAACCTCAATGGGCAGTACCTGCGCGGTGCGCACGCCTCCTATGCCGACGGC 808

Qy       1303 GTGGAGTGGTCCTCCTGGACCGGCTGGCAGTACTCACTCAAGTTCTCTGAGATGAAGATC 1362
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Db        809 GTGGAGTGGTCCTCCTGGACCGGCTGGCAGTACTCACTCAAGTTCTCTGAGATGAAGATC 868
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B

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Qy       1363 CGGCCGGTCCGGGAGGACCGCTAGACTGGTGCACCTTGTCCTTGGCCCTGCTGGTCCCTG 1422
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Db        869 CGGCCGGTCCGGGAGGACCGCTAGACCGGTGCACCTTGTCCTTGGCCCTGCTGGTCCCTG 928

Qy       1423 TCGCCCCATCCCCGACCCCACCTCACTCTTTCGTGAATGTTCTCCACCCACCTGTGCCTG 1482
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Qy       1483 GCGGACCCACTCTCCAGTAGGGAGGGGCCGGGCCATCCCTGACACGAAGCTCCCTGGGCC 1542
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Qy       1543 GGTGAAGTCACACATCGCCTTCTCGCCGTCCCCACCCCCTCCATTTGGCAG 1593
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